

<110> Kaneka Corporation

<120> NOVEL CARBONYL REDUCTASE, GENE THEREFOR, AND METHOD OF USING THE SAME

<130> T609HOP-GT

<150> JP2000-232756

<151> 2000-08-01

<160> 11

<210> 1

<211> 277

<212> PRT

<213> Micrococcus luteus

<400> 1

Met Arg Arg Met Thr Leu Pro Ser Gly Glu Ser Ile Pro Val Leu Gly

1 5 10 15

Gln Gly Thr Trp Gly Trp Gly Glu Asp Pro Gly Arg Arg Gly Asp Glu

20 25 30

Val Ala Ala Leu His Ala Gly Leu Glu Leu Gly Met Thr Leu Val Asp

35 40 45

Thr Ala Glu Met Tyr Ala Asp Gly Gly Ala Glu Glu Val Ala Gly Glu

50 55 60

Ala Leu Ala Gly Arg Arg Asp Glu Ala Phe Val Val Ser Lys Val Met

65 70 75 80

Pro Ser His Ala Ser Arg Ser Gly Thr Ile Ala Ala Cys Glu Arg Ser

85 90 95

Leu Lys Arg Leu Gly Thr Asp Arg Ile Asp Leu Tyr Leu Leu His Trp

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100	105	110
Gln Gly Arg Tyr Pro Leu Gln Asp Thr Val Ala Ala Phe His Gln Leu		
115	120	125
Val Glu Asp Gly Lys Ile Arg Tyr Trp Gly Val Ser Asn Phe Asp His		
130	135	140
Arg Ala Leu Ala Glu Leu Gln Asp Val Pro Gly Thr Ser Gly Leu Thr		
145	150	155
Thr Asp Gln Val Leu Tyr Asn Leu Ser Arg Arg Gly Pro Glu Tyr Asp		
165	170	175
Leu Leu Pro Trp Cys Ala Asp His Gln Leu Pro Val Met Ala Tyr Ser		
180	185	190
Pro Ile Glu Gln Gly Arg Ile Leu Asp Asp Thr Thr Leu Asn Asp Val		
195	200	205
Ala Ala Arg His Ser Val Ser Pro Ala Ala Ala Leu Ala Trp Val		
210	215	220
Leu Arg Arg Asp Ser Leu Cys Thr Ile Pro Lys Ala Ser Ser Pro Gln		
225	230	235
His Val Arg Asp Asn Ala Thr Ala Leu Asp Val Glu Leu Thr Arg Glu		
245	250	255
Asp Leu Asp Ala Leu Asp Arg Ala Phe Pro Pro Pro Ser Gly Pro Arg		
260	265	270
Pro Leu Glu Met Leu		
275		

<210> 2

<211> 834

<212> DNA

<213> Micrococcus luteus

<400> 2

atg cga cgg atg acg ctg ccg agt ggg gag tcc atc cct gtg ctg ggc
Met Arg Arg Met Thr Leu Pro Ser Gly Glu Ser Ile Pro Val Leu Gly

1 5 10 15

cag ggc acc tgg ggc tgg ggt gag gac ccc ggc cgc cgc ggc gac gag
Gln Gly Thr Trp Gly Trp Gly Glu Asp Pro Gly Arg Arg Gly Asp Glu

20 25 30

gtc gcc gcg ctg cac gcc ggc ctc gag ctg ggc atg acg ctg gtc gac
Val Ala Ala Leu His Ala Gly Leu Glu Leu Gly Met Thr Leu Val Asp

35 40 45

acc gcc gag atg tac gcc gac ggc ggt gcg gag gag gtg gct ggt gaa
Thr Ala Glu Met Tyr Ala Asp Gly Gly Ala Glu Glu Val Ala Gly Glu

50 55 60

gca ttg gcg ggt cgc cgc gac gag gcg ttc gtg gtc agc aag gtc atg
Ala Leu Ala Gly Arg Arg Asp Glu Ala Phe Val Val Ser Lys Val Met

65 70 75 80

ccg tcc cac gcc tcc cgt tcc ggc acg atc gcg gcc tgc gaa cgc agc
Pro Ser His Ala Ser Arg Ser Gly Thr Ile Ala Ala Cys Glu Arg Ser

85 90 95

ctg aaa cgc ctg ggc acc gat cgg atc gac ctc tac ctg ctg cac tgg
Leu Lys Arg Leu Gly Thr Asp Arg Ile Asp Leu Tyr Leu Leu His Trp

100 105 110

cag ggc agg tac ccg ctg cag gac acc gtc gcg gcc ttc cac cag ctc
Gln Gly Arg Tyr Pro Leu Gln Asp Thr Val Ala Ala Phe His Gln Leu

115 120 125

gtc gag gac ggg aaa atc cga tac tgg ggc gtc agc aac ttc gac cac
Val Glu Asp Gly Lys Ile Arg Tyr Trp Gly Val Ser Asn Phe Asp His

130 135 140

cgg gcc ctc gcc gag ctg cag gac gtg ccg ggc acc agc ggg ctg acc
 Arg Ala Leu Ala Glu Leu Gln Asp Val Pro Gly Thr Ser Gly Leu Thr
 145 150 155 160

acg gat cag gtg ctg tac aac ctg tcg ccg cga gga ccg gag tac gac
 Thr Asp Gln Val Leu Tyr Asn Leu Ser Arg Arg Gly Pro Glu Tyr Asp
 165 170 175

ctg ctg ccg tgg tgc gcc gac cac cag ctg ccg gtc atg gcg tac tcg
 Leu Leu Pro Trp Cys Ala Asp His Gln Leu Pro Val Met Ala Tyr Ser
 180 185 190

ccg atc gag cag ggc cgc atc ctt gac gac acg acg ctg aac gac gtc
 Pro Ile Glu Gln Gly Arg Ile Leu Asp Asp Thr Thr Leu Asn Asp Val
 195 200 205

gcg gcc cgt cac agc gtc agc ccc gcg gcg gcg gcc ctt gcc tgg gtg
 Ala Ala Arg His Ser Val Ser Pro Ala Ala Ala Leu Ala Trp Val
 210 215 220

ctg cgc cgc gac tcg ctc tgc acg atc ccc aag gcg agc agc ccg cag
 Leu Arg Arg Asp Ser Leu Cys Thr Ile Pro Lys Ala Ser Ser Pro Gln
 225 230 235 240

cac gtg cgc gac aac gcc aca gca ctg gac gtg gag ctg acc cgc gaa
 His Val Arg Asp Asn Ala Thr Ala Leu Asp Val Glu Leu Thr Arg Glu
 245 250 255

gac ctg gat gct ctg gac cgt gcg ttt ccg ccc ccg agc gga ccg cga
 Asp Leu Asp Ala Leu Asp Arg Ala Phe Pro Pro Pro Ser Gly Pro Arg
 260 265 270

cca ctg gaa atg ctg tga
 Pro Leu Glu Met Leu
 275

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 3

gayaengcng aratgtaygc

20

<210> 4

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 4

tcytcnacna gytgrtgraa

20

<210> 5

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 5

gcgcatatgc gacggatgac gctgcc

26

<210> 6

<211> 32

<212> DNA

<213> Artificial Sequence

<220>

<400> 6

32

<211> 46

<213> Artificial Sequence

<223> Description of Artificial Sequence: primer

46

<211> 29

⟨213⟩ Artificial Sequence

<223> Description of Artificial Sequence: primer

29

<211> 144

<213> Artificial Sequence

<223> Description of Artificial Sequence: double-stranded DNA

60

120

gctgctttac atgctggtct cgag

<210> 10

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 10

caggagctct aaggaggta acaatgtata aag

33

<210> 11

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 11

cacggatcct tatccgcgtc ctgcttgg

28

